FIGURE 1

A.

SEQ ID NO:1 - Hu1 light chain variable region amino acid sequence

EIVLTQSPDFQSVTPKEKVTITCRASQFVGSSIHWYQQKPDQSPKLLIKYASESMS
GVPSRFSGSGSGTDFTLTINSLEAEDAATYYCQQSHSWHFTFGQGTKVEIK

B.

SEQ ID NO:2 - Hu1 light chain variable region nucleic acid sequence

GAAATTGTGCTGACTCAGTCTCCAGACTTTCAGTCTGTGACTCCAAAAGAGA
AAGTCACCATCACCTGCAGGGCCAGTCAGTTCGTTGGCTCAAGCATCCACTG
GTACCAGCAGAAGCCAGATCAGTCTCCAAAGCTCCTCATCAAGTATGCTTCT
GAGTCTATGTCTGGGGTCCCCTCGAGGTTCAGTGGCAGTGGATCTGGGACAG
ATTTCACCCTCACCATCAATAGCCTGGAAGCTGAAGATGCTGCCACGTATTAC
TGTCAACAAAGTCATAGCTGGCATTTCACGTTCGGCCAAGGGACCAAGGTGG
AAATCAAA

FIGURE 2

A.

SEQ ID NO:3 - Hu1 heavy chain variable region amino acid sequence

EVQLVESGGGLVQPGGSLRLSCAASGFTFSNHWMNWVRQAPGKGLEWVGEIRS
KSINSATHYAESVKGRFTISRDDSKNSLYLQMNSLKTEDTAVYYCARNYYGSTY
DHWGQGTLVTVSS

B.

SEQ ID NO:4 - Hu1 heavy chain variable region nucleic acid sequence

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGAGGGTCCC
TGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTCAGTAACCACTGGATGAAC
TGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTGGCGAAATTAGAT
CAAAATCTATTAATTCTGCAACACATTATGCGGAGTCTGTGAAAGGGAGATT
CACCATCTCAAGAGATGATTCAAAGAACTCACTGTACCTGCAGATGAACAGC
CTGAAAACCGAGGACACGGCCGTGTATTACTGTGCTAGAAATTACTACGGTA
GTACCTACGACCATTGGGGCCAAGGGACCCTGGTCACCGTCTCCTCA

FIGURE 3

A.

SEQ ID NO:5 - A10K light chain variable region amino acid sequence

EIVLTQSPDFQSVTPKEKVTITCRASQFVGYSIHWYQQKPDQSPKLLIKYASESRS
GVPSRFSGSGSGTDFTLTINSLEAEDAATYYCQQSHSWHFTFGQGTKVEIK

B.

SEQ ID NO:6 - A10K light chain variable region nucleic acid sequence

GAAATTGTGCTGACTCAGTCTCCAGACTTTCAGTCTGTGACTCCAAAAGAGA
AAGTCACCATCACCTGCAGGGCCAGTCAGTTCGTTGGCTATAGCATCCACTG
GTACCAGCAGAAGCCAGATCAGTCTCCAAAGCTCCTCATCAAGTATGCTTCT
GAGTCTAGGTCTGGGGTCCCCTCGAGGTTCAGTGGCAGTGGATCTGGGACAG
ATTTCACCCTCACCATCAATAGCCTGGAAGCTGAAGATGCTGCCACGTATTAC
TGTCAACAAAGTCATAGCTGGCATTTCACGTTCGGCCAAGGGACCAAGGTGG
AAATCAAA

FIGURE 4

A.

SEQ ID NO:7 - A10K heavy chain amino acid sequence

EVQLVESGGGLVQPGGSLRLSCAASGFKFSNHWMNWVRQAPGKGLEWVGEIRS
KSMNSATHYAESVKGRFTISRDDSKNSLYLQMNSLKTEDTAVYYCARNYYGST
YDHWGQGTLVTVSS

B.

SEQ ID NO:8 - A10K heavy chain nucleic acid sequence

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGAGGGTCCC
TGAGACTCTCCTGTGCAGCCTCTGGATTCCCTTTCAGTAACCACTGGATGAAC
TGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTGGCGAAATTAGAT
CAAAATCTATGAATTCTGCAACACATTATGCGGAGTCTGTGAAAGGGAGATT
CACCATCTCAAGAGATGATTCAAAGAACTCACTGTACCTGCAGATGAACAGC
CTGAAAACCGAGGACACGGCCGTGTATTACTGTGCTAGAAATTACTACGGTA
GTACCTACGACCATTGGGGCCAAGGGACCCTGGTCACCGTCTCCTCA

FIGURE 5

A.   **Amino acid sequence of a human light chain framework region with interspersed CDR sequences labeled**

(FRL1 - SEQ ID NO:57)   (CDRL1)   (FRL2 - SEQ ID NO:58)   (CDRL2)
EIVLTQSPDFQSVTPKEKVTITC<u>XXXXXXXXXXX</u>WYQQKPDQSPKLLIK<u>XXXXXXX</u>

(FRL3 - SEQ ID NO:59)   (CDRL3)   (FRL4 - SEQ ID NO:60)
GVPSRFSGSGSGTDFTLTINSLEAEDAATYYC<u>XXXXXXXXX</u>FGQGTKVEIK

B.   **Nucleic acid sequence of a human light chain framework region with interspersed CDR sequences labeled**

'(FRL1 - SEQ ID NO:61)
GAAATTGTGCTGACTCAGTCTCCAGACTTTCAGTCTGTGACTCCAAAAGAGAAAG

                                                (CDRL1)
TCACCATCACCTGC<u>XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX</u>TGGTAC

(FRL2 - SEQ ID NO:62)   (CDRL2)
CAGCAGAAGCCAGATCAGTCTCCAAAGCTCCTCATCAAG<u>XXXXXXXXXXXXXXX</u>

(CDRL2 cont.)   (FRL3 - SEQ ID NO:63)
<u>XXXXXXX</u>GGGGTCCCCTCGAGGTTCAGTGGCAGTGGATCTGGGACAGATTTCAC

CCTCACCATCAATAGCCTGGAAGCTGAAGATGCTGCCACGTATTACTGT

                (CDRL3)   (FRL4 - SEQ ID NO:64)
<u>XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX</u>TTCGGCCAAGGGACCAAGGTGGAAA

TCAAA

FIGURE 6

A.   Amino acid sequence of a human heavy chain framework region with interspersed CDR sequences labeled

```
      (FRH1 - SEQ ID NO:65)                (CDRH1)        (FRH2 - SEQ ID NO:66)
EVQLVESGGGLVQPGGSLRLSCAASXXXXXXXXXXXWVRQAPGKGLEWVG

              (CDRH2)                          (FRH3 - SEQ ID NO:67)
XXXXXXXXXXXXXXXXXXXXXXXRFTISRDDSKNSLYLQMNSLKTEDTAVYYCAR

      (CDRH3)      (FRH4 - SEQ ID NO:68)
XXXXXXXXXWGQGTLVTVSS
```


B.   Nucleic acid sequence of a human heavy chain framework region with interspersed CDR sequences labeled

```
                   (FRH1 - SEQ ID NO:69)
GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGAGGGTCCCTG

                                       (CDRH1)
AGACTCTCCTGTGCAGCCTCTXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTG

         (FRH2 - SEQ ID NO:70)                        (CDRH2)
GGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTGGCXXXXXXXXXXXXXX

                   (CDRH2 cont.)
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXAGATTCAC

         (FRH3 - SEQ ID NO:71)
CATCTCAAGAGATGATTCAAAGAACTCACTGTACCTGCAGATGAACAGCCTGAA

                                         (CDRH3)
AACCGAGGACACGGCCGTGTATTACTGTGCTAGAXXXXXXXXXXXXXXXXXXXXX

   (CDRH3)              (FRH4 - SEQ ID NO:72)
XXXXXXXXXTGGGGCCAAGGGACCCTGGTCACCGTCTCCTCA
```
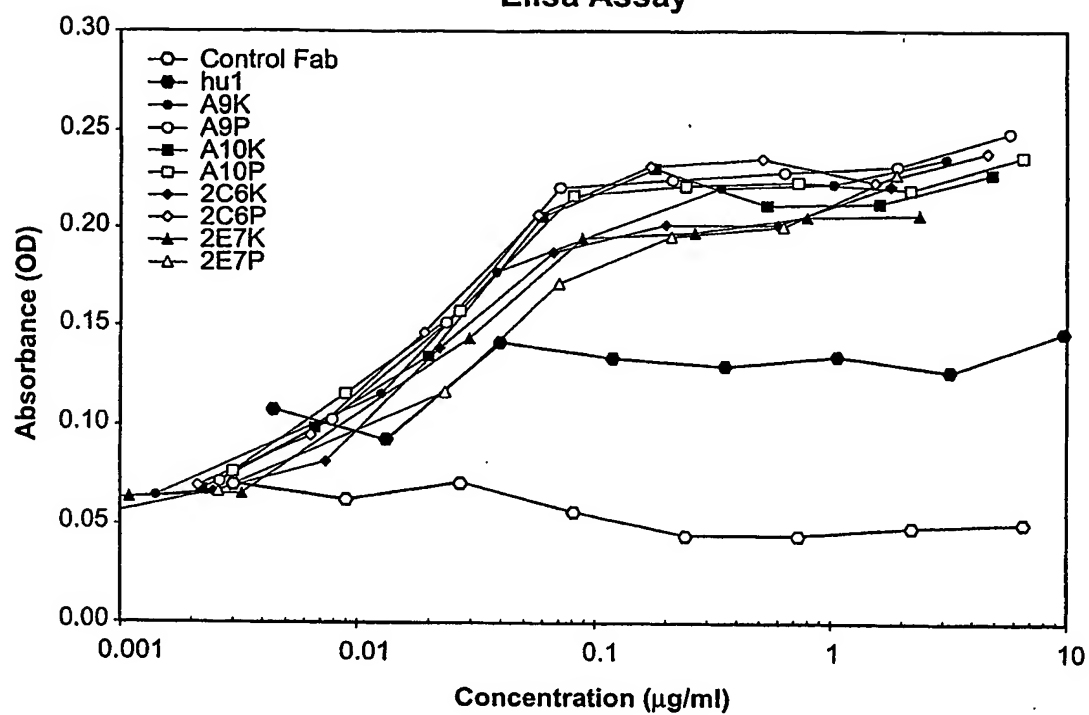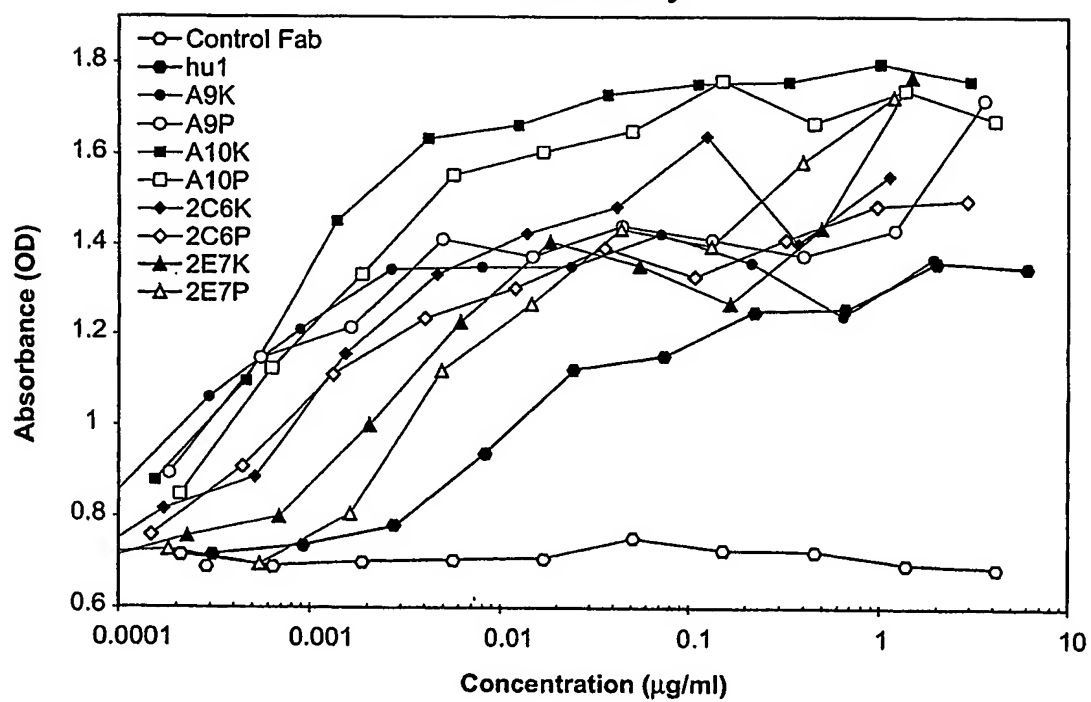
FIGURE 7

Elisa Assay
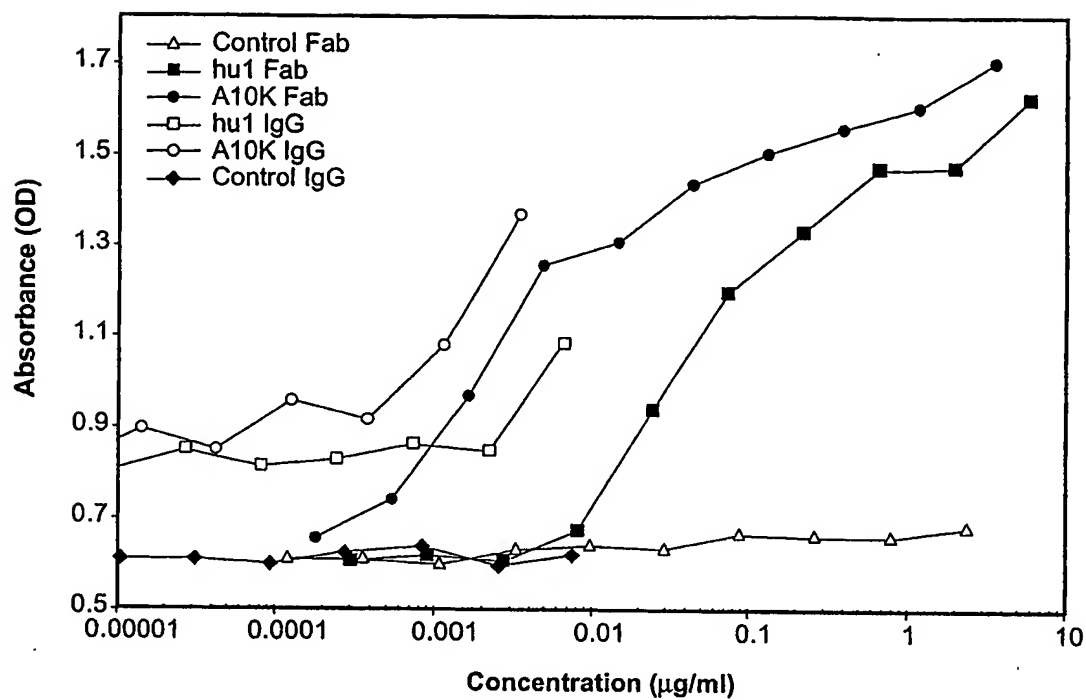
FIGURE 8

L929 Assay

FIGURE 9
L929 Assay

FIGURE 10

L929 Assay
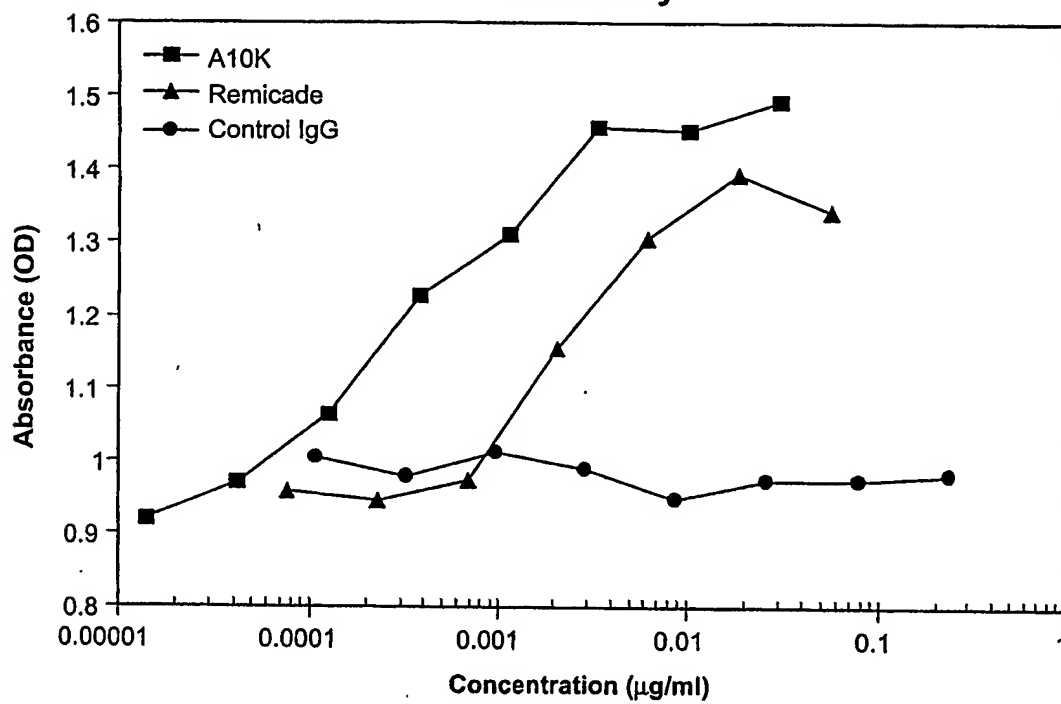
FIGURE 11
Lethality Model
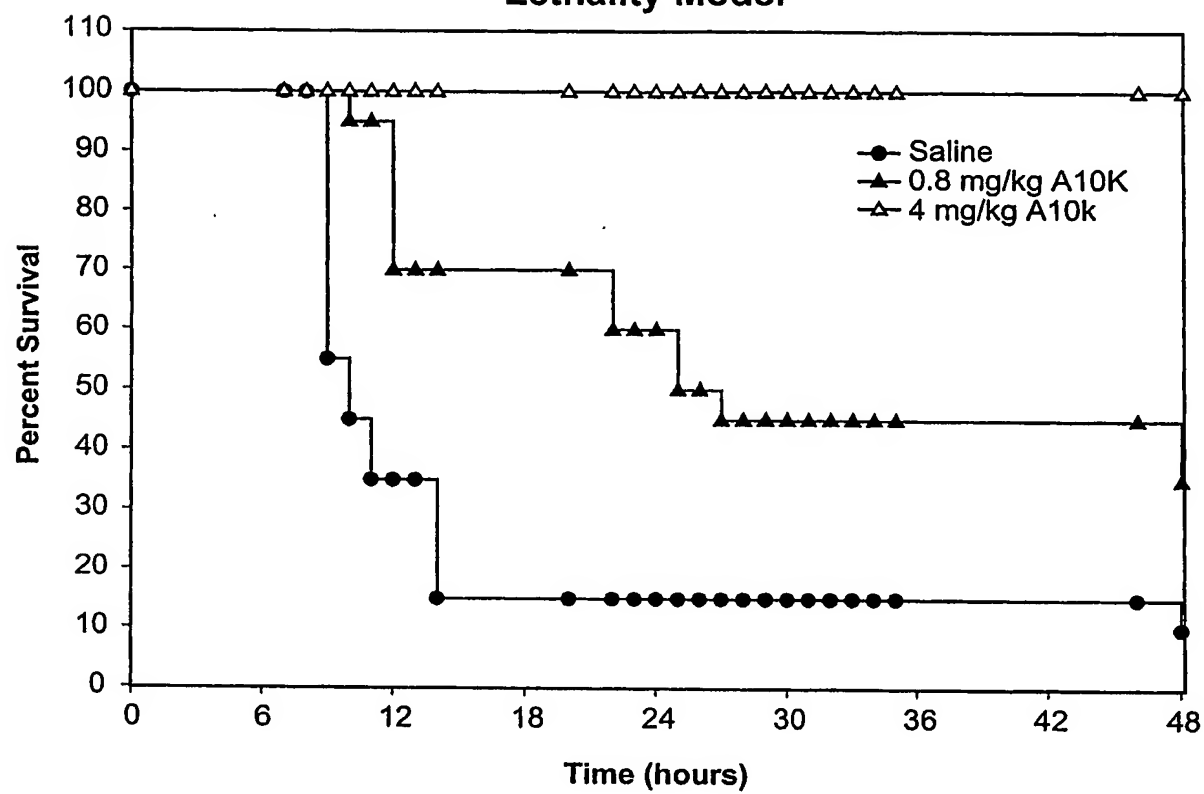
FIGURE 12
Polyarthritis Model

FIGURE 13

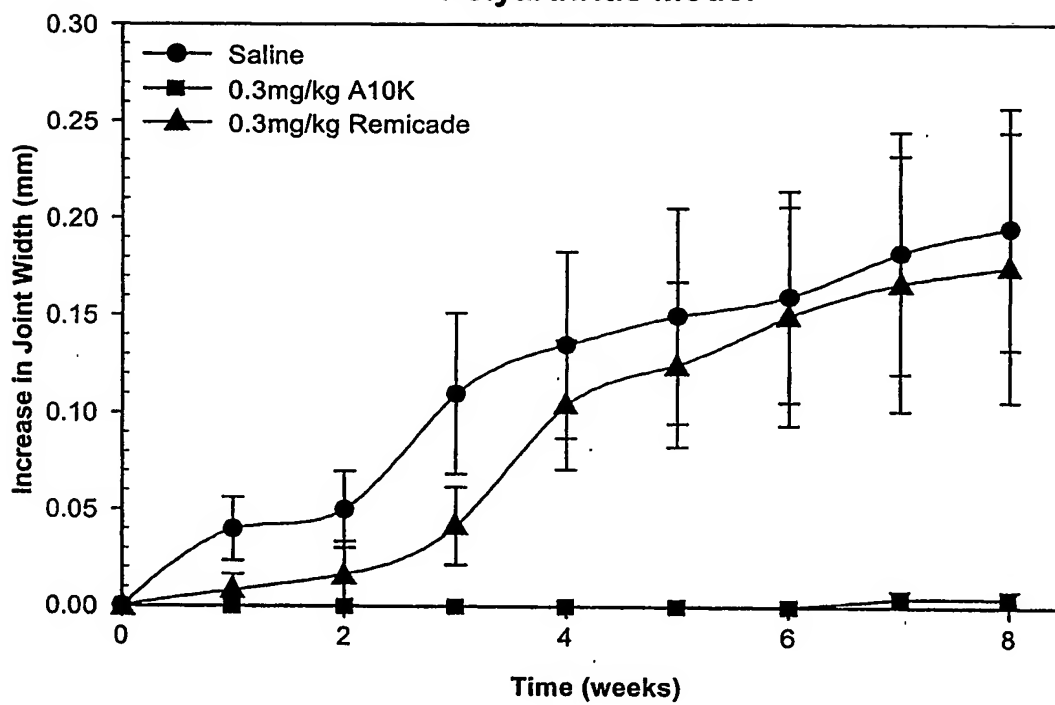|		
▭	domains	
⋀⋀	inter-domain sections	
—	disulphide bonds	
V	variable	
C	constant	
L	light chain	
H	heavy chain	

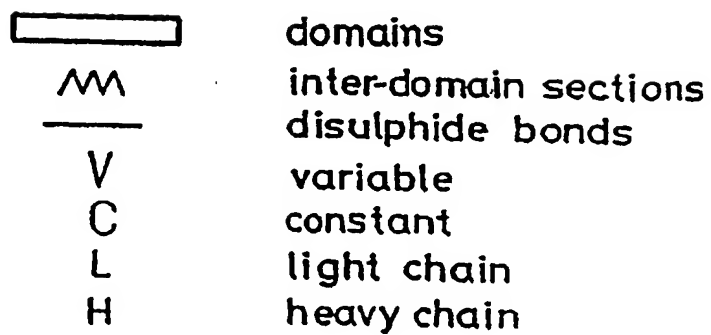# FIGURE 14

A.   SEQ ID NO:85 - Human CL Sequence

TCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAG
CACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC
GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACA
CCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTG
ACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATC
ACAAGCCCAGCAACACCAAGGTGGACAAGAAA**GCAGAGCCCAAATCTTCT**
<u>ACTAGTGTTCTC</u>*TACCCATATGATGTACCTGATTATGCATCA*TAG

Note: This CH1 sequence contains the first six IgG1 hinge region residues (in bold) and fused to a HA decapeptide tag (italic) through a four amino acid linker (underlined).

B.   SEQ ID NO:86 - Human CH1 Sequence

CGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTT
GAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAG
AGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCA
GGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAG
CACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGC
GAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGG
GAGAGTCTTAG

FIGURE 15

A.

SEQ ID NO:109 - AME 3-2 Complete Heavy Chain

EVQLVESGGGLVQPGGSLRLSCAASGFTFRNHWMNWVRQAPGKGLEWVGEIR
SKSINSATFYAESVKGRFTISRDDSKNSLYLQMNSLKTEDTAVYYCARNYYGSY
YDHWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVD
KRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH
EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS
DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH
EALHNHYTQKSLSLSPGK*

B.

SEQ ID NO:110 - AME 3-2 Complete Light Chain

DIQMTQSPSSLSASVGDRVTITCVTTQFVGYAIHWYQQKPGKAPKLLIYYASSSR
SGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHGWPFTFGQGTKVEIKRTV
AAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVT
EQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC*